



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 130284

TO: Manjunath N Rao
Location: REM-2A01&2c70
Art Unit: 1652
Wednesday, August 25, 2004

Case Serial Number: 10/059447

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*

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Search Notes

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2004, 18:57:25 ; Search time 0.537723 Seconds
(without alignments)
677.842 Million cell updates/sec

Title: US-10-059-447B-6

Perfect score: 32

Sequence: 1 IILLKEP 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	90.6	101	1	GLRX_CHICK
2	28	87.5	467	1	PCXA_ANASP
3	28	87.5	1640	1	CO3_ONCMY
4	28	87.5	2560	1	PPS2_BACSU
5	27	84.4	227	1	COMB_THEMA
6	27	84.4	307	1	K1PF_BORBU
7	27	84.4	517	1	T2FA_HUMAN
8	27	84.4	574	1	STR_BUCAL
9	27	84.4	1245	1	NARZ_ECOLI
10	26	81.2	180	1	Y047_METUA
11	26	81.2	207	1	Y078_METUA
12	26	81.2	261	1	SUHB_NELMA
13	26	81.2	266	1	CEMA_CHLVU
14	26	81.2	269	1	TFIS_MORSP
15	26	81.2	332	1	MDHC_ARATH
16	26	81.2	332	1	MDHC_BETVU
17	26	81.2	332	1	MDHC_MAIZE
18	26	81.2	332	1	MDHC_MESCA
19	26	81.2	332	1	MDHC_MESCR
20	26	81.2	332	1	MDHD_ARATH
21	26	81.2	332	1	YIEZ_HSVB4
22	26	81.2	413	1	SVH_FUSN
23	26	81.2	429	1	RNE_GUTH
24	26	81.2	504	1	CEA5_DROME
25	26	81.2	576	1	YITO_YEAST
26	26	81.2	600	1	NUCD_BUCAL
27	26	81.2	630	1	GATE_METUA
28	26	81.2	647	1	NTP1_MSEPV
29	26	81.2	837	1	LZTR_MOUSE
30	26	81.2	840	1	LZTR_HUMAN
31	26	81.2	914	1	GUX2_CLOSR
32	26	81.2	918	1	CAPP_CORGL
33	26	81.2	919	1	CAPP_CORCT

ALIGNMENTS

RESULT 1

GLRX_CHICK STANDARD; PRT; 101 AA.

AC P79764;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glutaredoxin (Thioltransferase) (Ttase).

GN GLRX OR GRX.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98334490; PubMed=9671415;

RA Goller M.E., Iacovoni J.S., Vogt P.K., Kruse U.;

RT "Glutaredoxin is a direct target of oncogenic jun.";

RL Oncogene 16:2945-2948(1998).

CC -!- FUNCTION: Has a glutathione-disulfide oxidoreductase activity in

the presence of NADPH and glutathione reductase. Reduces low

molecular weight disulfides and proteins.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the glutaredoxin family.

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CC EMBL; Y09235; CAA70437.1; -

DR HSSP; P35754; LJHB.

DR InterPro; IPR002109; Glutaredoxin.

DR Pfam; PF00462; Glutaredoxin; 1.

DR PRINTS; PR00160; GLUTAREDOXIN.

DR PROSITE; PS00195; GLUTAREDOXIN; 1.

KW Redox-active center; Electron transport.

FT DISULFID 23 26 REDOX-ACTIVE (BY SIMILARITY).

SQ SEQUENCE 101 AA; 11397 MW; 50619DBE15456F2 CRC64;

Query Match

Best Local Similarity 90.6%; Score 29; DB 1; Length 101;

Matches 5; Conservative 71.4%; Pred. No. 8.6;

Mismatches 2; Indels 0; Gaps 0;

QY 1 IILLKEP 7

DB 30 IILLKEP 36

RESULT 2

PCXA_ANASP STANDARD; PRT; 467 AA.

ID PCXA_ANASP